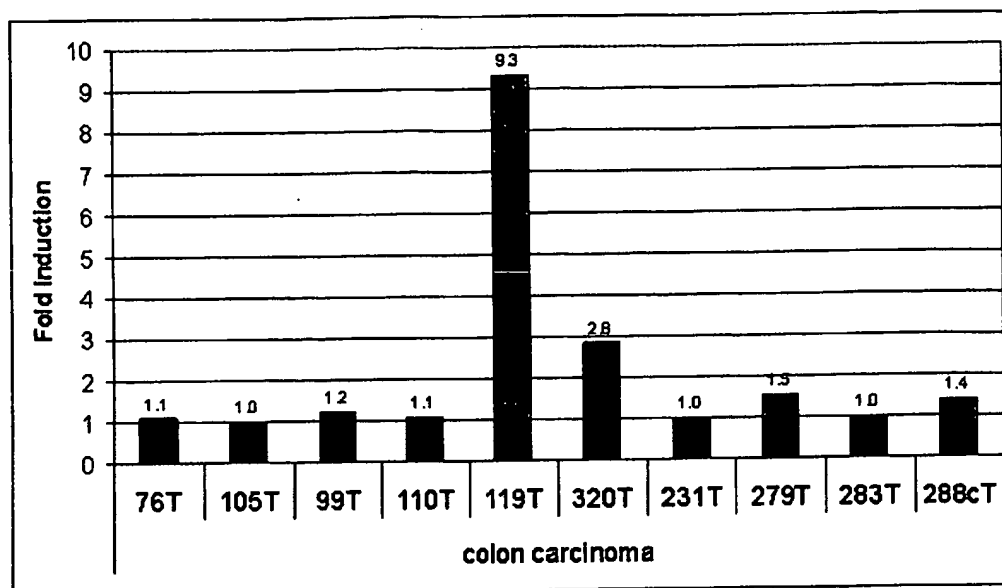
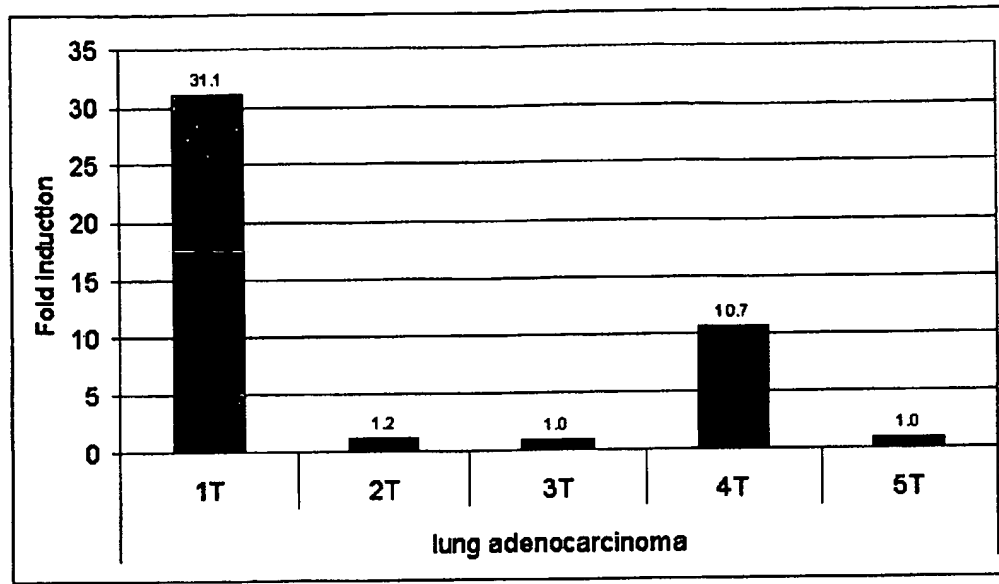


Figure 1:



TKT-L1

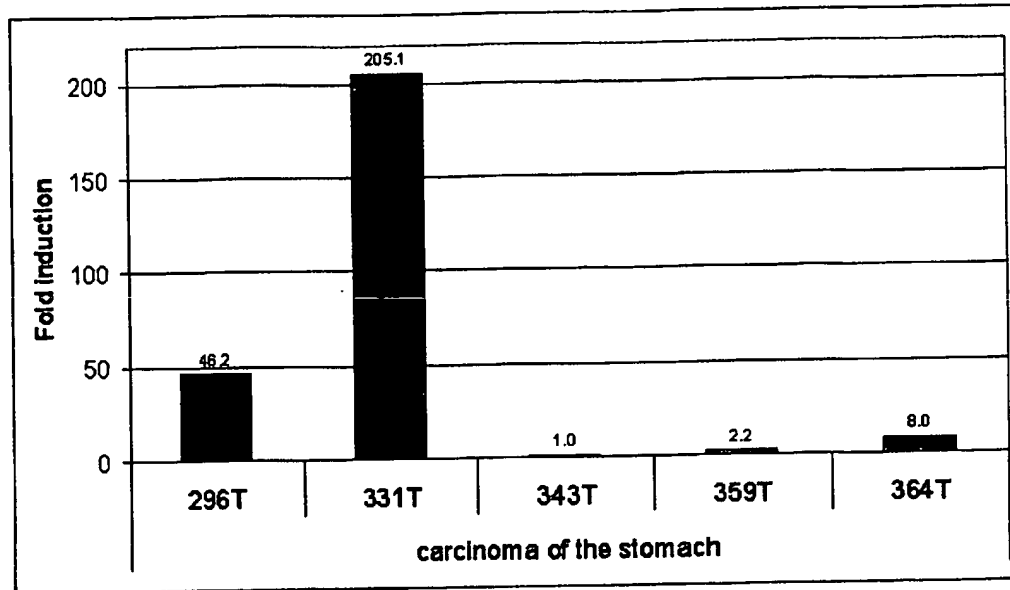
Figure 2:



TKT-L1

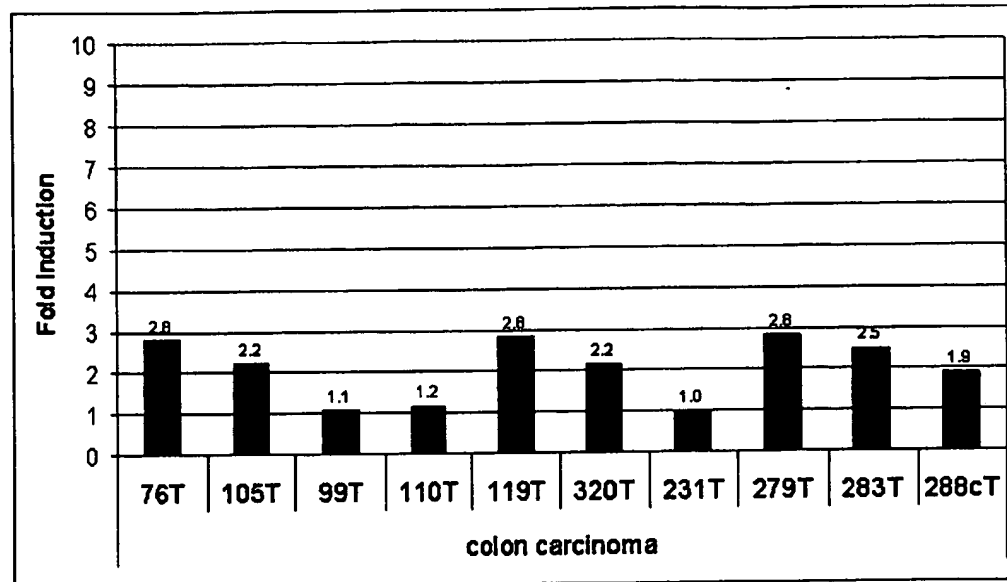
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Figure 3:



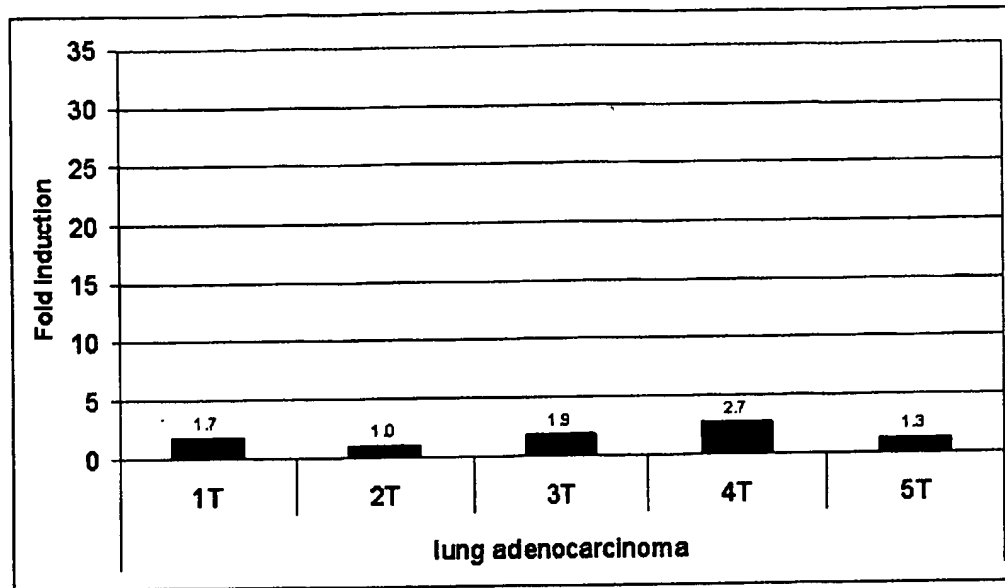
TKT-L1

Figure 4:



TKT

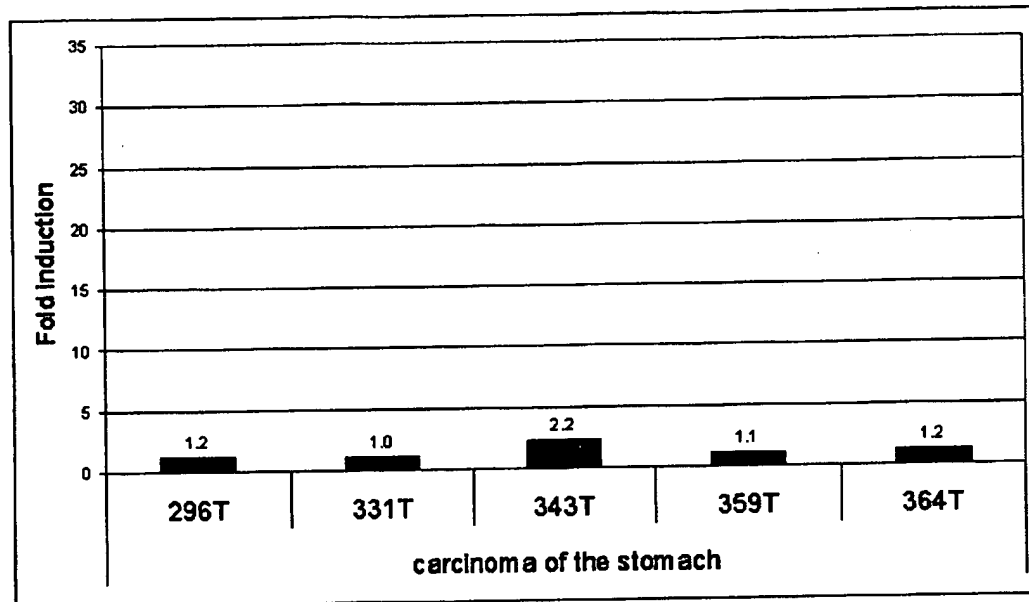
Figure 5:



TKT

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Figure 6



TKT

Fig. 7: DNA and amino acid sequence of TKT-L1

1 GCCATTGCTCTTCAGACGCCGGAGACGTAGGAGTGGGTCTTCAGACTCCAAAGGGGTTG
61 GACTAATGGCGGATGCTGAGGCGAGGGCTGAGTTCCTCGAGGAGGCCAGACCTGACAGGG
M A D A E A R A E F P E E A R P D R G
121 GCACCTTGCAGGTGTTGCAAGATATGGCCAGCCGCTTGCGAATCCATTCCATCAGGGCCA
T L Q V L Q D M A S R L R I H S I R A T
181 CATGCTCCACGAGCTCCGGCCACCCTACATCATGTAGCAGTTCTTCTGAGATCATGTCTG
C S T S S G H P T S C S S S S E I M S V
241 TGCTGTCTTCTACATCATGAGGTACAAGCAGTCAGATCCAGAGAATCCGGACAACGACC
L F F Y I M R Y K Q S D P E N P D N D R
301 GATTTGTCCTCGCAAAGAGACTGTGCTTGTGGATGTGGCAACAGGATGGCTCGGACAAG
F V L A K R L S F V D V A T G W L G Q G
361 GACTGGGAGTTGCATGTGGAATGGCATATACTGGCAAGTACTTCGACAGGGCCAGCTACC
L G V A C G M A Y T G K Y F D R A S Y R
421 GGGTGTCTGCCTCATGAGTGATGGCGAGTCTCAGAAGGCTCTGTCTGGGAGGCAATGG
V F C L M S D G E S S E G S V W E A M A
481 CCTTTGCTTCCTACTACAGTCTGGACAATCTTGTGGCAATCTTTGATGTGAACCGCCTGG
F A S Y Y S L D N L V A I F D V N R L G
541 GACACAGTGGTGCATTGCCCCCGAGCACTGCATAAACATCTATCAGAGGCGCTGCGAAG
H S G A L P A E H C I N I Y Q R R C E A
601 CCTTTGGGTGGAACACTTATGTGGTGGACGGCCGGGACGTGGAGGCACTGTGCCAGGTAT
F G W N T Y V V D G R D V E A L C Q V F
661 TCTGGCAGGCTTCTCAGGTGAAGCACAAGCCCACTGCTGTGGTGGCCAAGACCTTCAAGG
W Q A S Q V K H K P T A V V A K T F K G
721 GCCGGGGCACCCCAAGTATTGAGGATGCAGAAAGTTGGCATGCAAAGCCAATGCCGAGAG
R G T P S I E D A E S W H A K P M P R E
781 AAAGAGCAGATGCCATTATCAAATTAATTGAGAGCCAGATACAGACCAGCAGGAATCTTG
R A D A I I K L I E S Q I Q T S R N L D
841 ACCCACAGCCCCCATTGAGGACTCACCTGAAGTCAACATCACAGATGTAAGGATGACCT
P Q P P I E D S P E V N I T D V R M T S
901 CTCCACCTGATTACAGAGTTGGTGACAAGATAGCTACTCGGAAAGCATGCGGTCTGGCTC
P P D Y R V G D K I A T R K A C G L A L
961 TGGCTAAGCTGGGCTACGCGAACAACAGAGTCGTTGTGCTGGATGGTGACACCAGGTA
A K L G Y A N N R V V V L D G D T R Y S
1021 CTACTTTCTCTGAGATATTCAACAAGGAGTACCCTGAGCGCTTCATCGAGTGCCTTATGG
T F S E I F N K E Y P E R F I E C F M A
1081 CTGAACAAAACATGGTGAGCGTGGCTCTGGGCTGTGCCTCCCGTGGACGGACCATGCTT
E Q N M V S V A L G C A S R G R T I A F
1141 TTGCTAGCACCTTTGCTGCCCTTCTGACTCGAGCATTTGATCACATCCGGATAGGAGGCC
A S T F A A F L T R A F D H I R I G G L

1201 TCGCTGAGAGCAACATCAACATTATTGGTTCCCACTGTGGGGTATCTGTTGGTGACGATG
A E S N I N I I G S H C G V S V G D D G

1261 GTGCTTCCCAGATGGCCCTGGAGGATATAGCCATGTTCCGAACCATTCCCAAGTGCACGA
A S Q M A L E D I A M F R T I P K C T I

1321 TCTTCTACCCAACTGATGCCGTCTCCACGGAGCATGCTGTTGCTCTGGCAGCCAATGCCA
F Y P T D A V S T E H A V A L A A N A K

1381 AGGGGATGTGCTTCATTCCGACCACCCGACCAGAACTATGGTTATTTACACCCCAACAG
G M C F I R T T R P E T M V I Y T P Q E

1441 AACGCTTTGAGATCGGACAGGCCAAGGTCCTCCGCCACTGTGTCAGTGACAAGGTCACAG
R F E I G Q A K V L R H C V S D K V T V

1501 TTATTGGAGCTGGAATTACTGTGTATGAAGCCTTAGCAGCTGCTGATGAGCTTTGAAAC
I G A G I T V Y E A L A A A D E L S K Q

1561 AAGATATTTTATCCGTGTCATCGACCTGTTTACCATTAAACCTCTGGATGTCGCCACCA
D I F I R V I D L F T I K P L D V A T I

1621 TCGTCTCCAGTGCAAAAGCCACAGAGGGCCGGATCATTACAGTGGAGGATCACTACCCGC
V S S A K A T E G R I I T V E D H Y P Q

1681 AAGGTGGCATCGGGGAAGCTGTCTGCGCAGCCGTCTCCATGGATCCTGACATTCAGGTTG
G G I G E A V C A A V S M D P D I Q V H

1741 ATTCGCTGGCAGTGTGGGAGTGCCCCAGAGTGGGAAGTCCGAGGAATTGCTGGATATGT
S L A V S G V P Q S G K S E E L L D M Y

1801 ATGGAATTAGTGCCAGACATATCATAGTGGCCGTGAAATGCATGTTGCTGAACTAAAATA
G I S A R H I I V A V K C M L L N *

1861 GCTGTTAGCCTTGGTCTTTTGGCCTCTTTACCCTGTGTTTATGTTTGTTCAAAACCATC

1921 ATTTAAATCTCTACTGTCACATTTTGTTCCTTAAAAGCAAAGCCAGCTAACACCTTCATT

1981 CATCCCTAGTTCGGAAATTCAAGCTAACTACTTACCCTTTAAACTGTCACTGCATATGCA

2041 AGTACCGCTCTAATTTTGGATCATTAAGGGAGTTACACAACCTTTAAGTGAAAAAAT

2101 AGGTAACAAAACAACACCTGATAGTAAGTTTCTGATAAGACTATAGATAAGTGGTAGA

2161 GGTAATCAATCTTCCGAAGTGTTCCTTCGTGAATAACTGGTAGAGGTAATAGTTTTTT

2221 CAATGTATTTCTTCATGAGTAAAGAAAATGTGGATTGAAGTATAGATTCCAGTAGCCTA

2281 GTTTCACAGCACGATAACACCATGACGCCTACTGCTGTTCCACCTTGGGATTCTGTGT

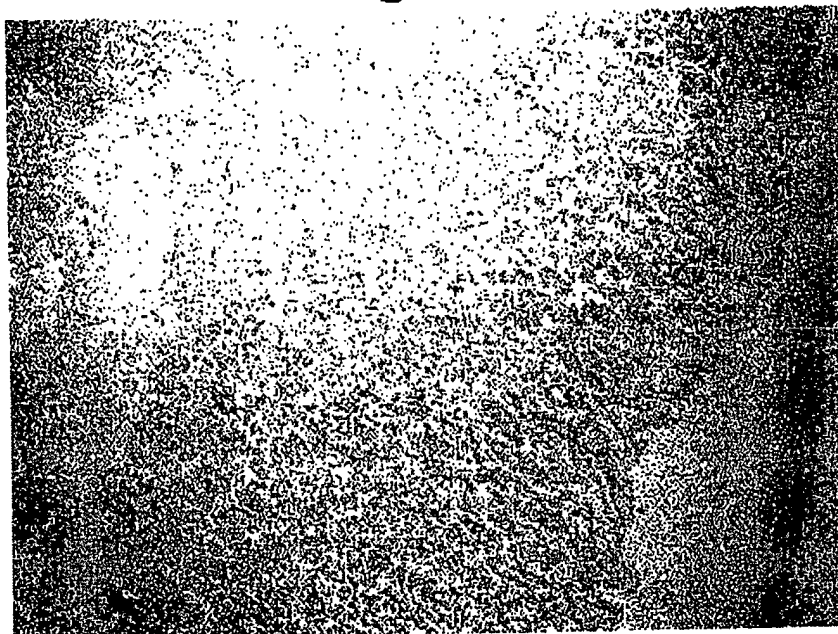
2341 GCTGCCATCCACCTGCAGCTGCCCTGGAATTCCTTCGCTGTTTGCCTTCATCTCCCTC

2401 CACGTTTGAGAGGCTGTCAGGCAGCAGCGAAAGCTGTAGGATGTCCTGTGCTGCTGTGT

2461 GATGAGAGCCTCCACACTGTACTGTTCAAGTCAATGTTAATAAAGCATTTCAAACCCAAA

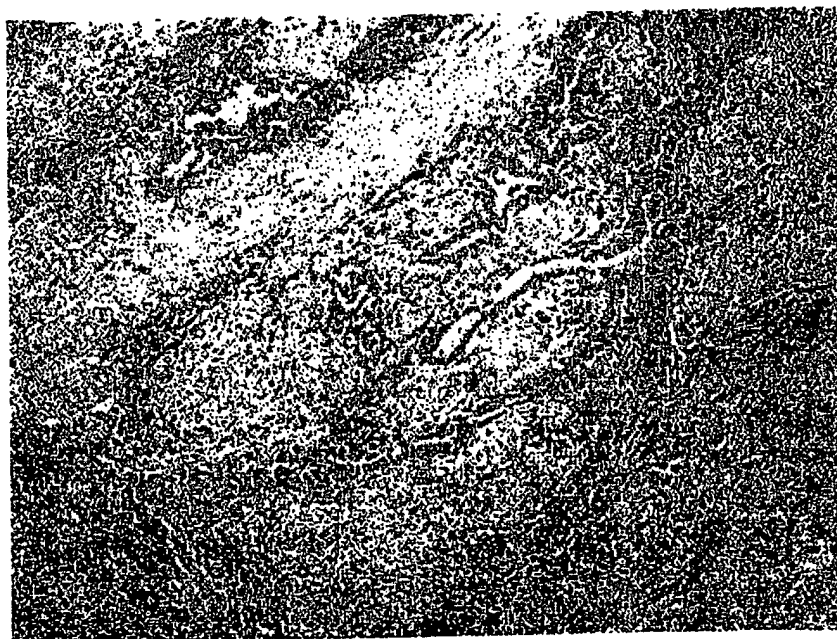
2521 AAAAAAAAAA

Fig. 8



A

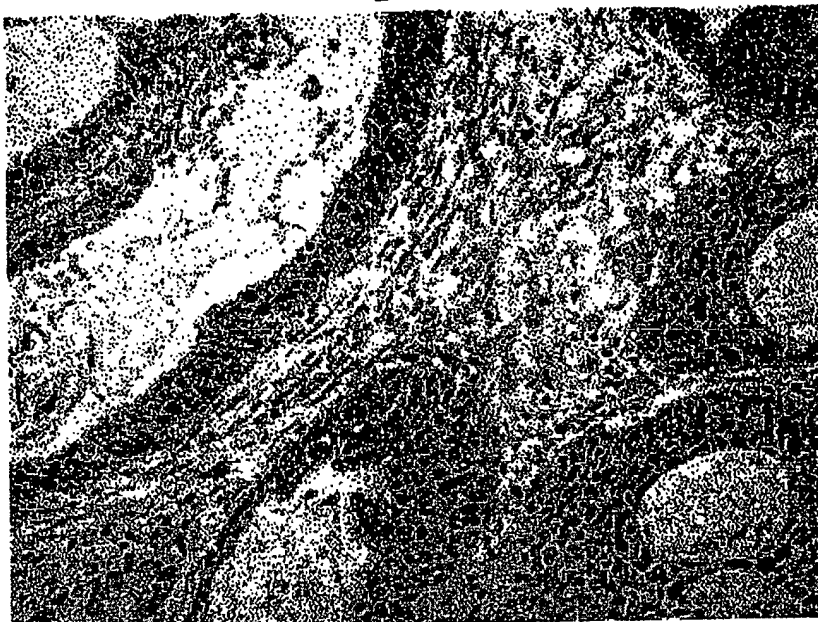
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B

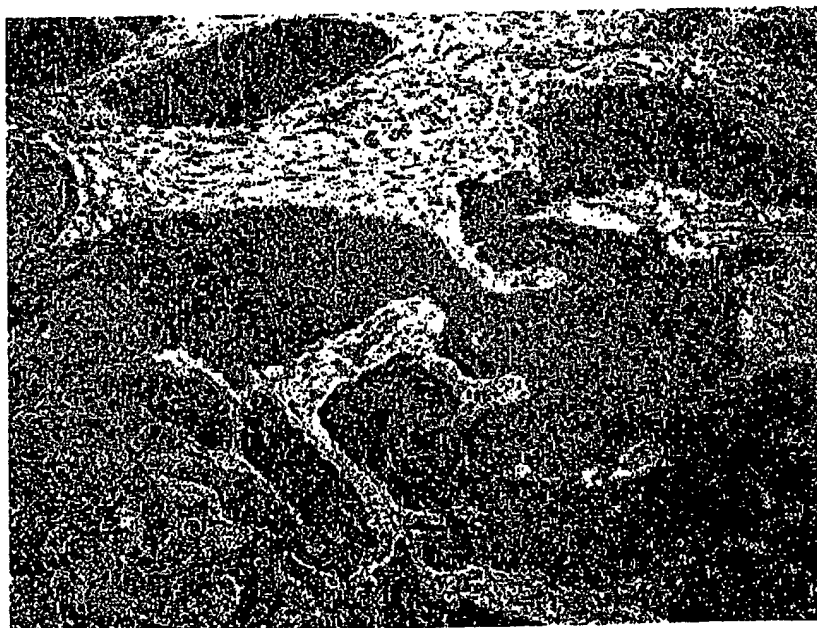
1666

Fig.9



A

1682



B

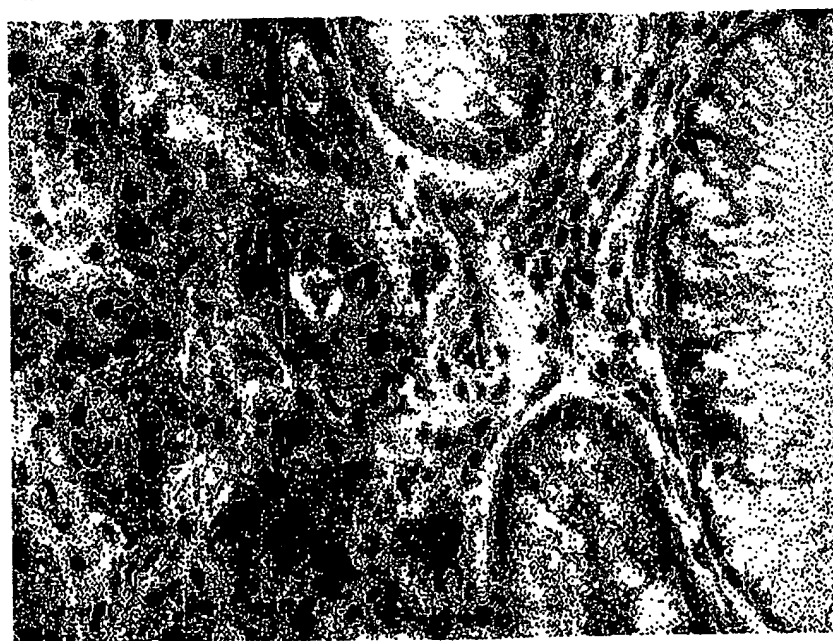
1697

Fig.10



A

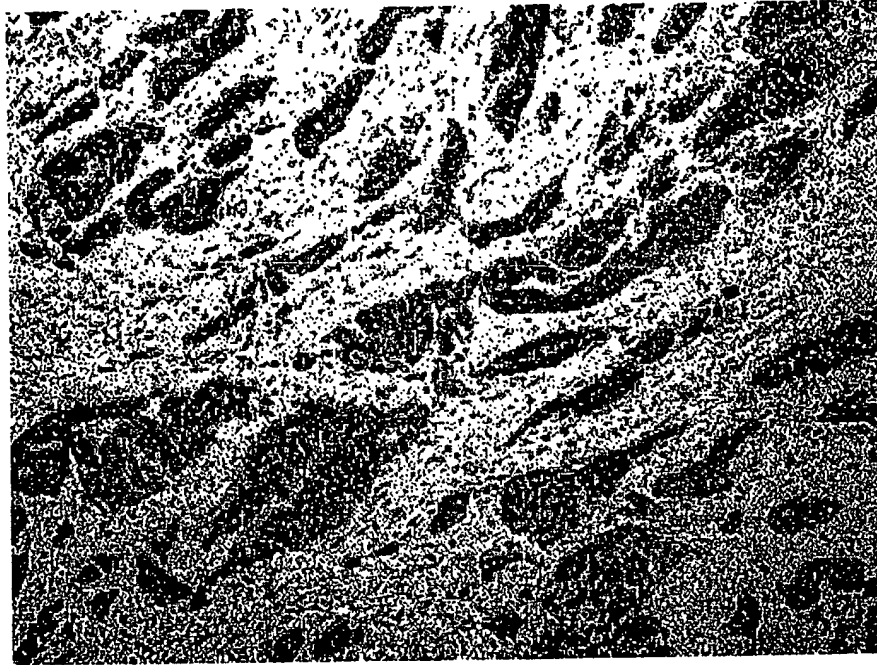
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B

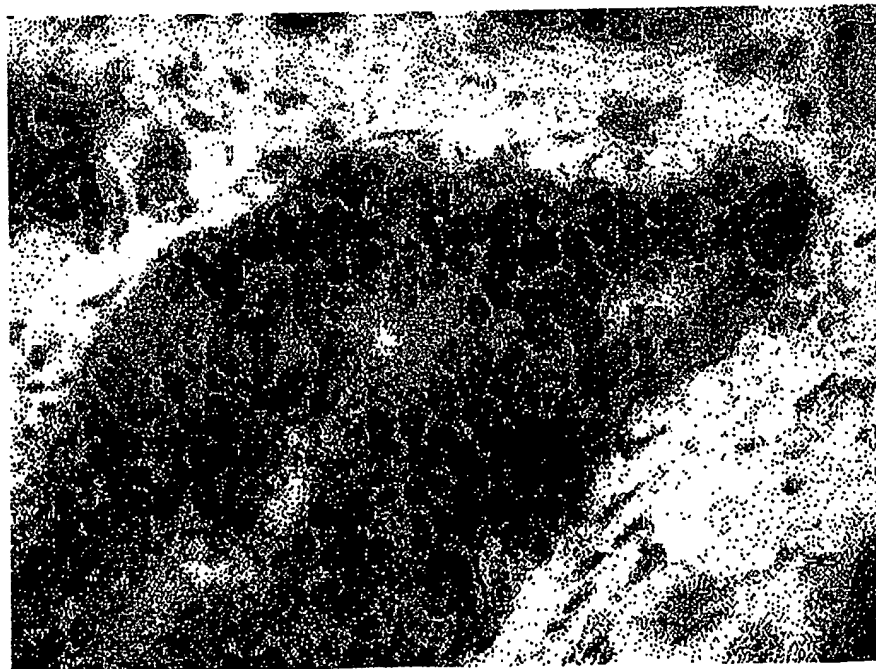
1699

Fig.11



A

1698



B

1698

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